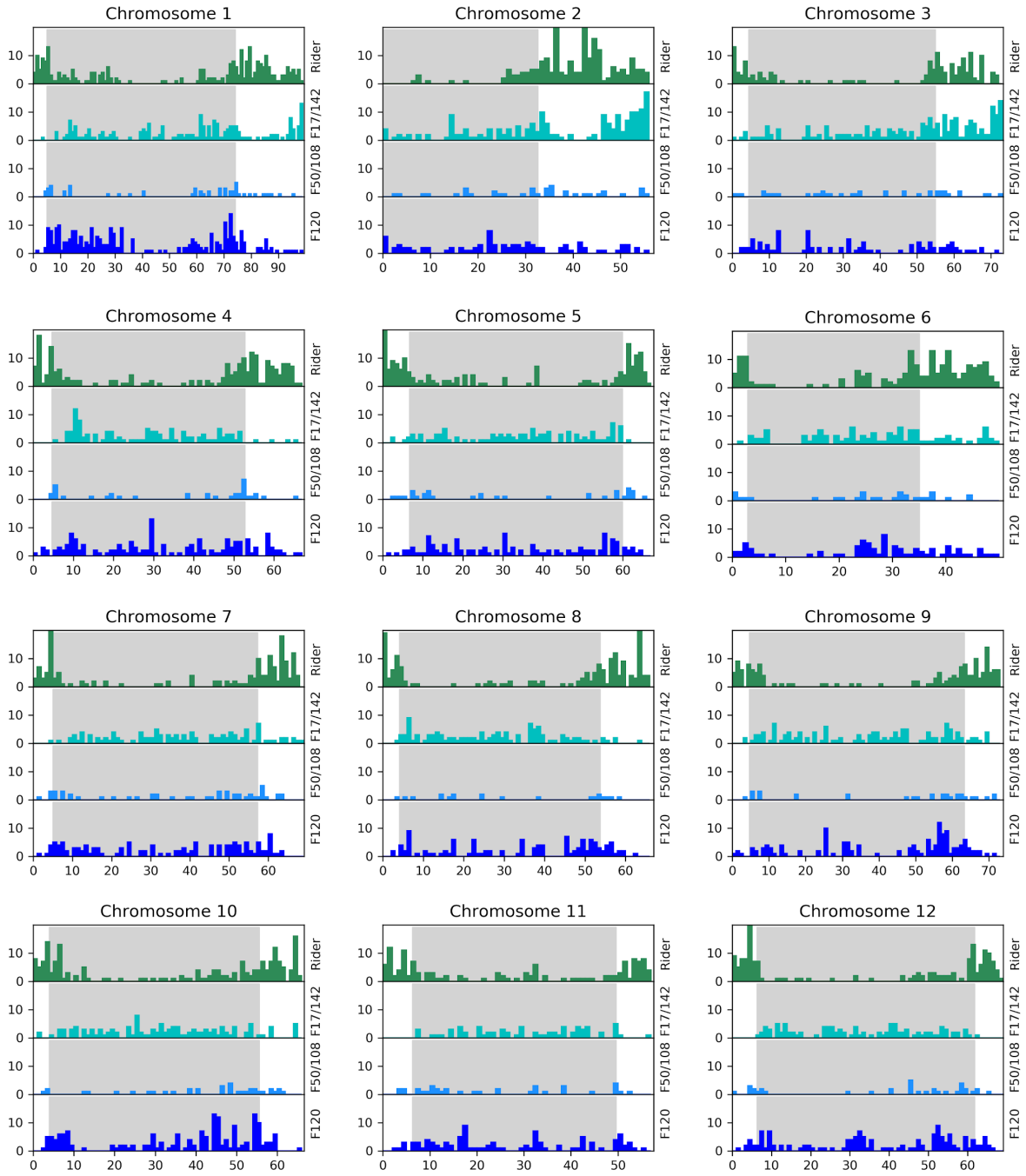

Figure S1. The distribution of insertions of four RT families along the genome. The height of the bars indicates the number of insertions in 1 Mb bins. The x-axis scale is in Mb. For visualization, the values on the y-axis are limited to 20, for the whole dataset see Data S1. The heterochromatin regions are shown as grey blocks.

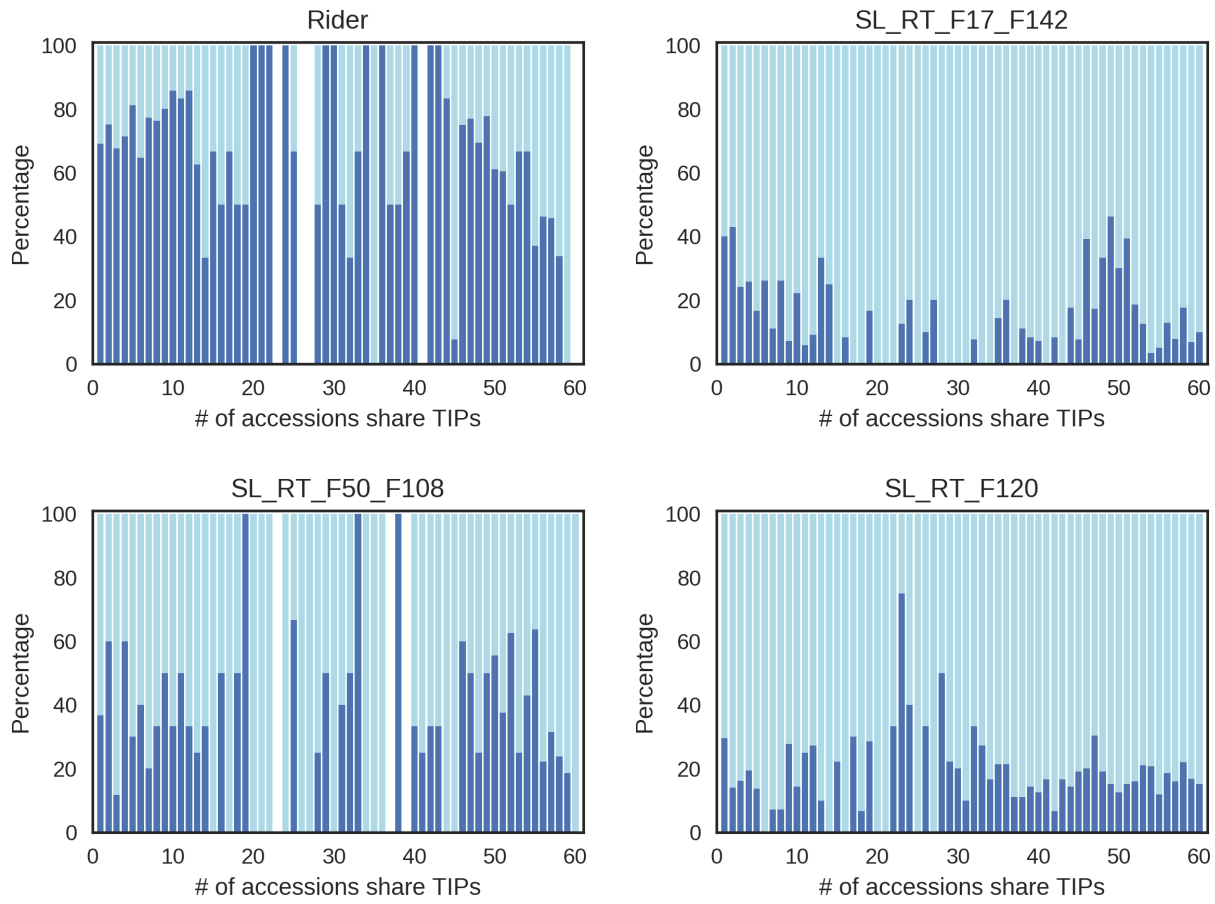

Figure S2. Stacked bar graphs of the RT insertion presence in euchromatin vs. heterochromatin in four families, as a function of the number of accessions sharing the insertions. The X-axis shows the number of accessions that share the same RT insertions. The graph represents the percentage of shared RT insertions in a given number of accessions on the x-axis. Light blue represents the percentage of insertions in heterochromatin and dark blue represents those in euchromatin. White spaces means there are no insertions shared by the corresponding number of accessions.

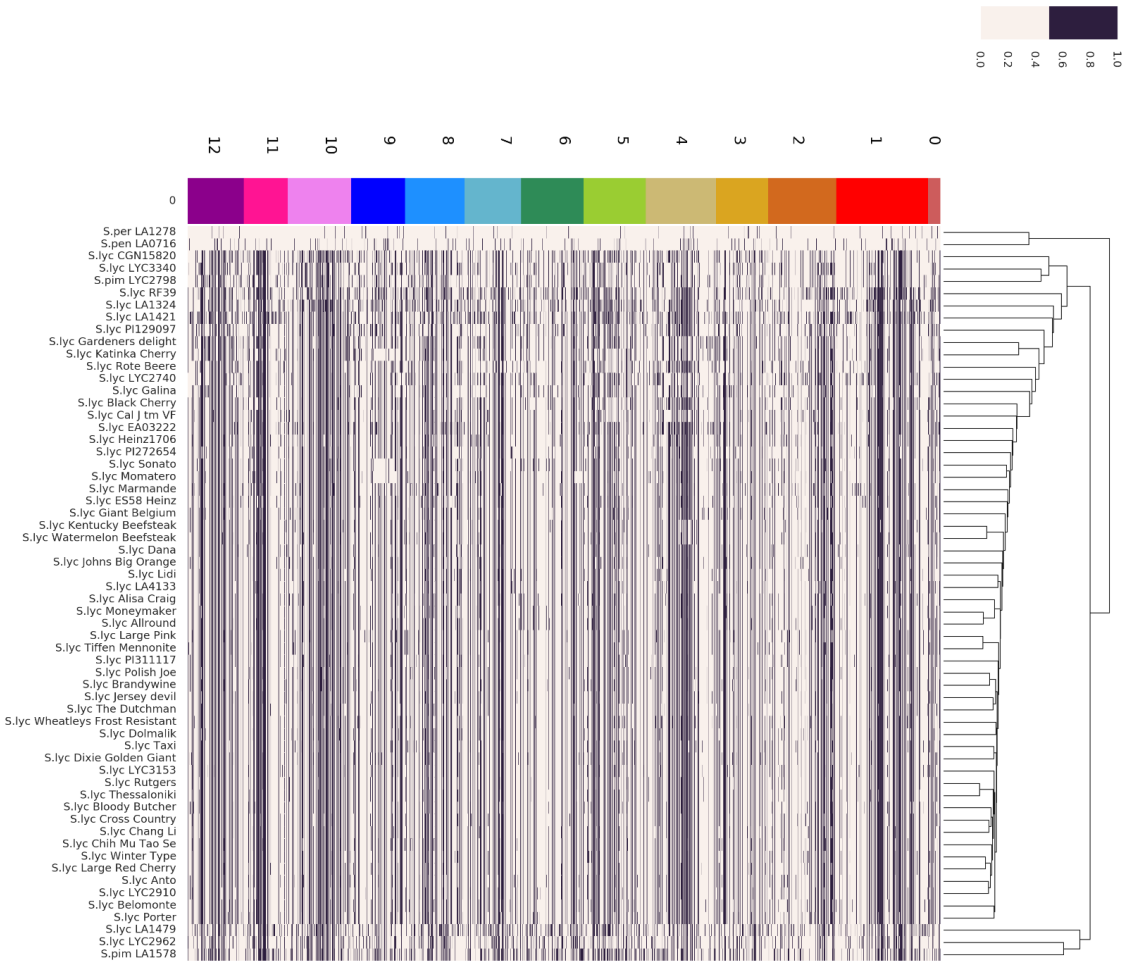

Fig. S3. Clustermap of *Rider* insertions, with insertions ordered by chromosome position. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

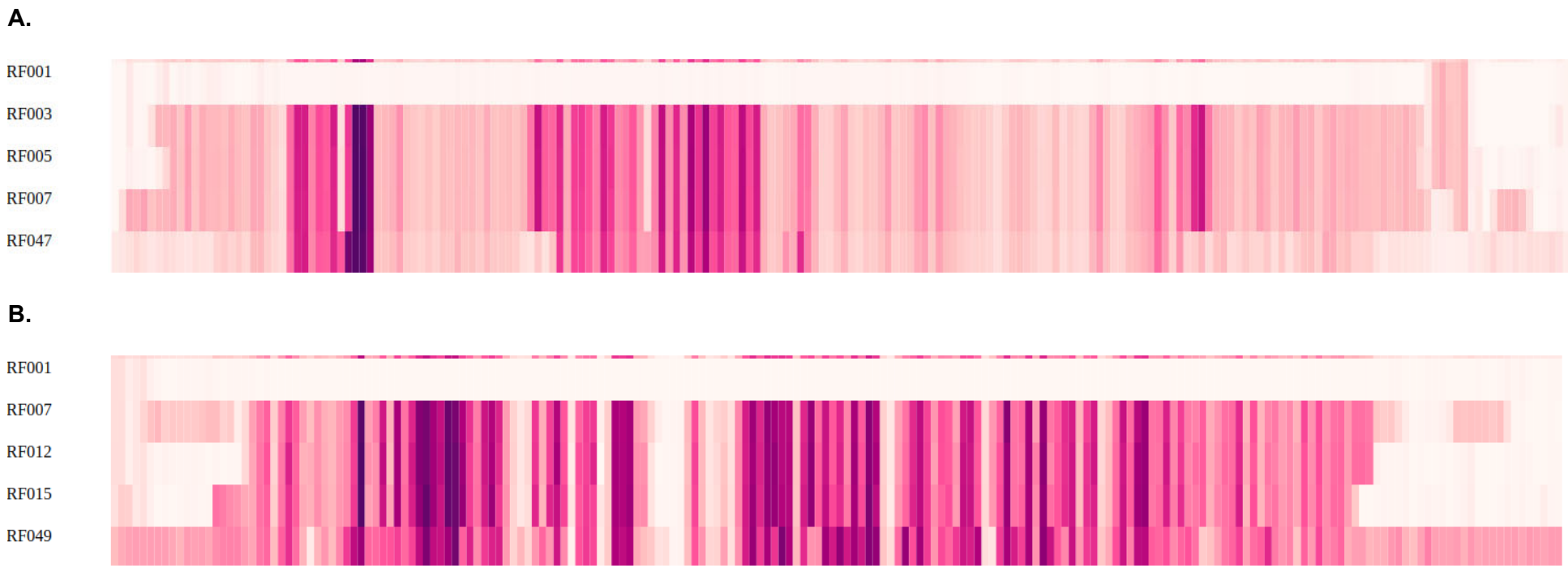

Fig. S4. SNP density in selected accessions compared with A. Chromosome 4 of *S. pimpinellifolium* (RF047) and B. Chromosome 9 of *S. peruvianum* (RF049). Both panels show cv. Moneymaker (RF001) as negative control at the top. Both chromosomes were divided in 200 equally sized bins.

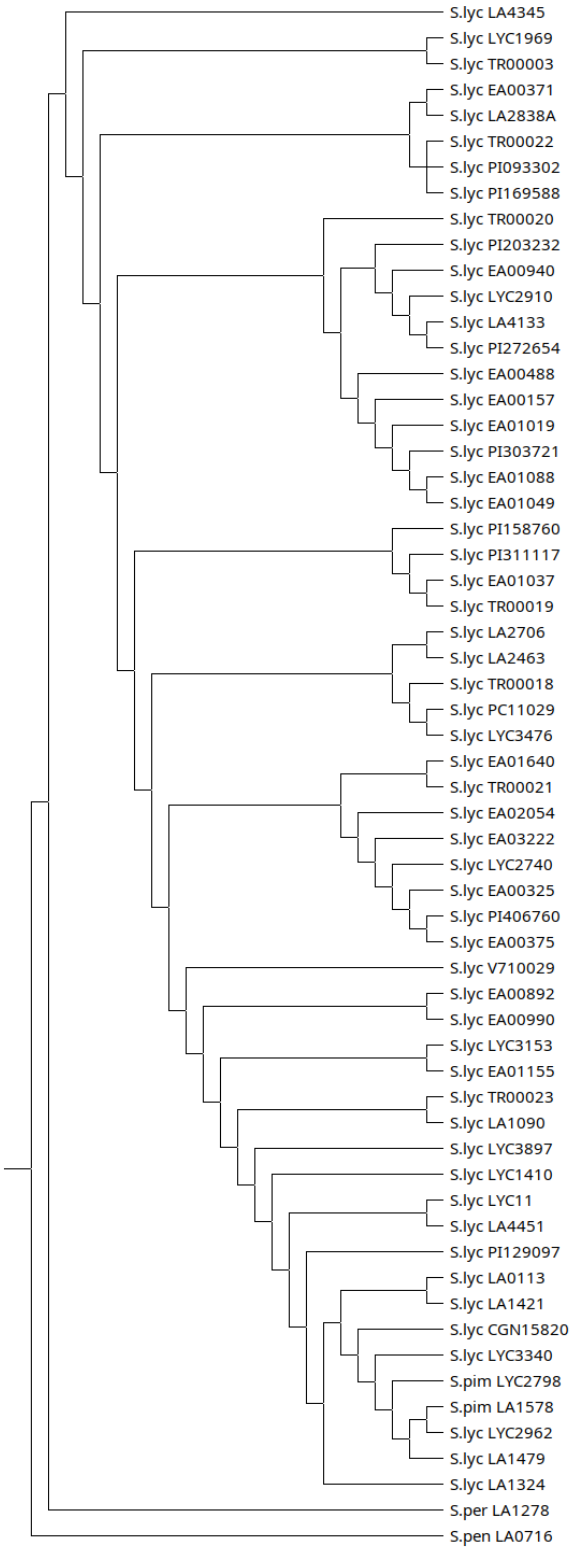

Figure S5. Whole genome SNP based phylogenetic tree reconstructed from Aflitos et al., 2014. The accession codes can be found in Table S3.

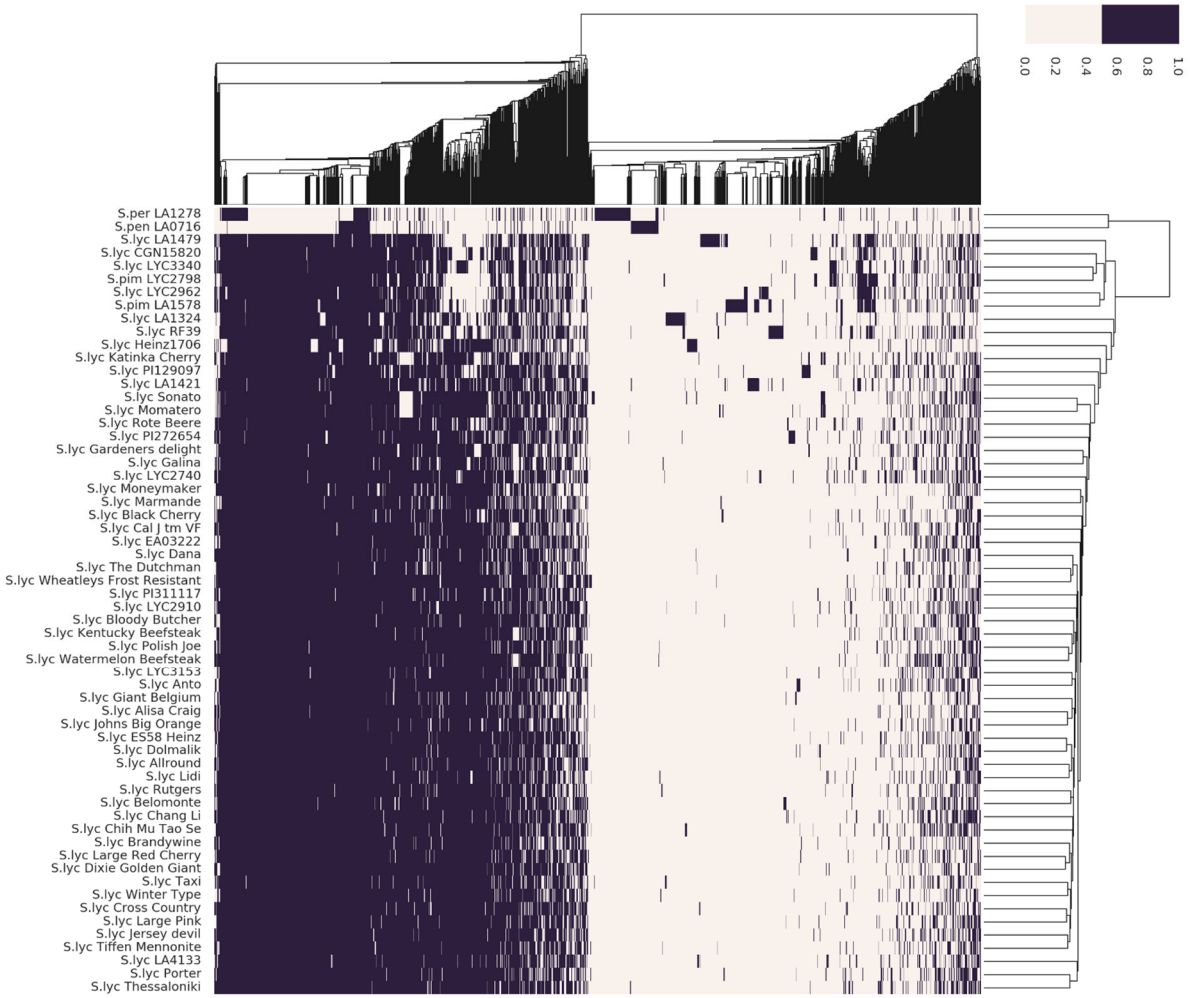

Fig. S6. Clustermap of RT_F17/142 insertions, with insertions clustered by Euclidian distance on the left. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

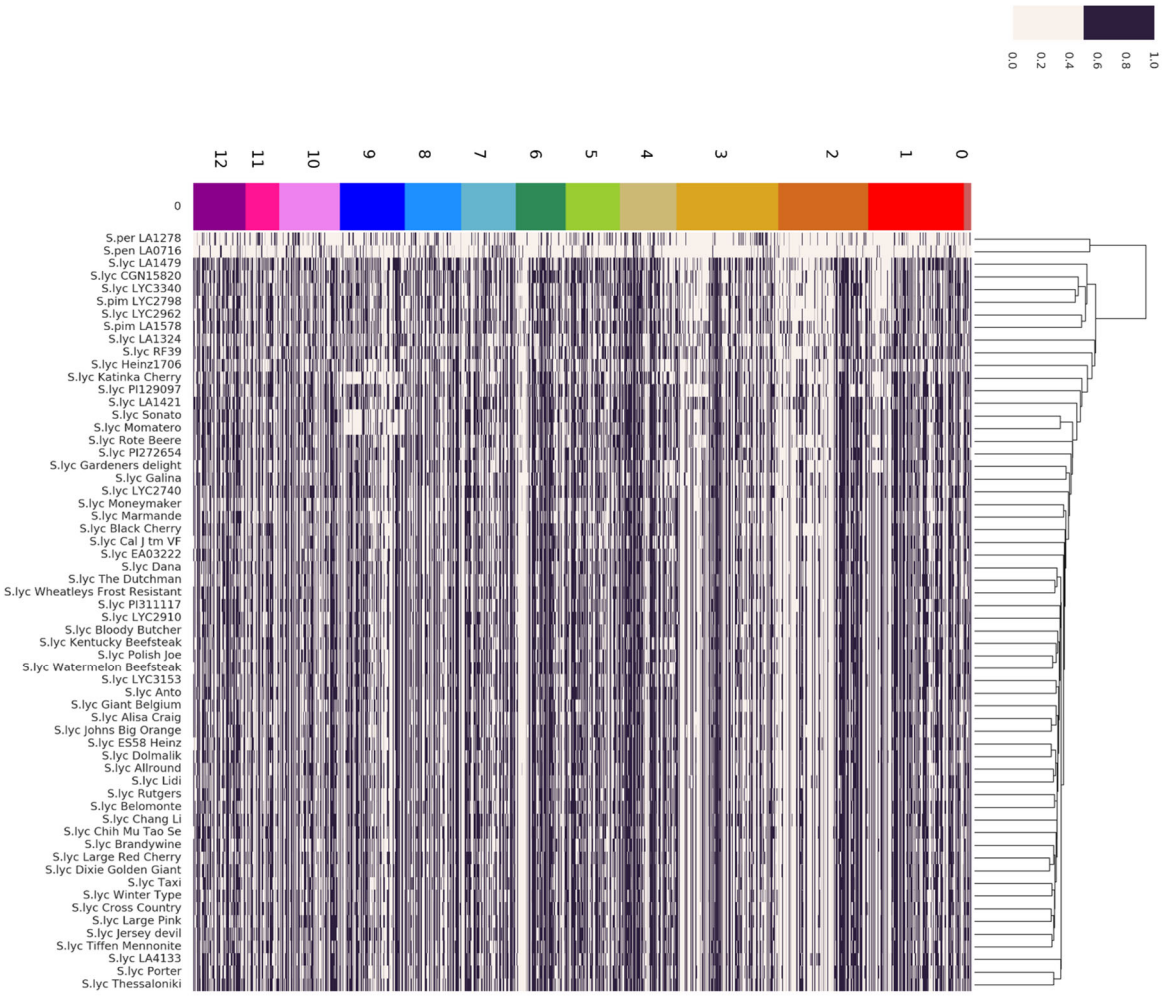

Fig. S7. Clustermap of RT17/142 insertions, with insertions ordered by chromosome position. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

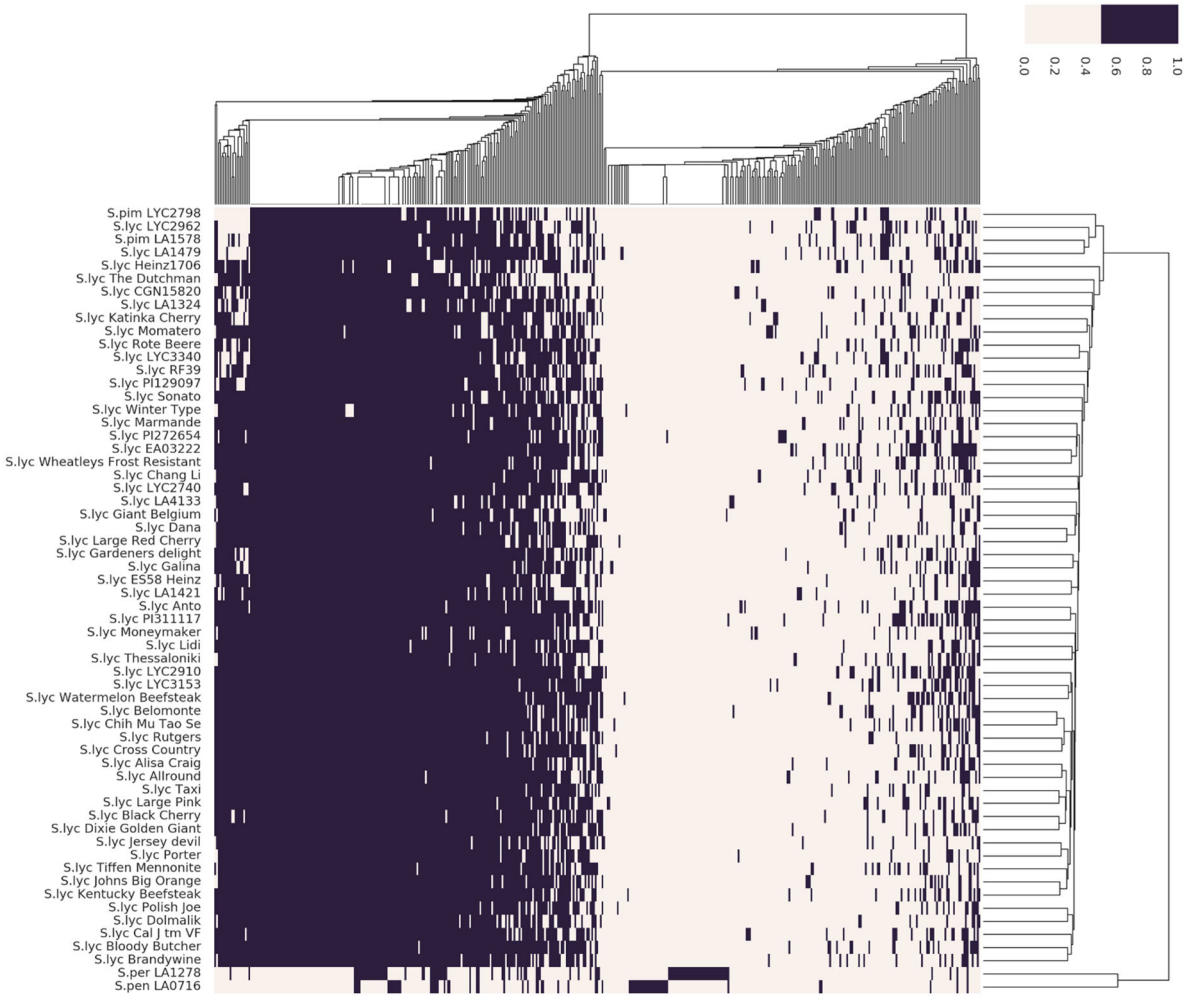

Fig. S8. Clustermap of RT_F50/108 insertions, with insertions clustered by Euclidian distance on the left. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

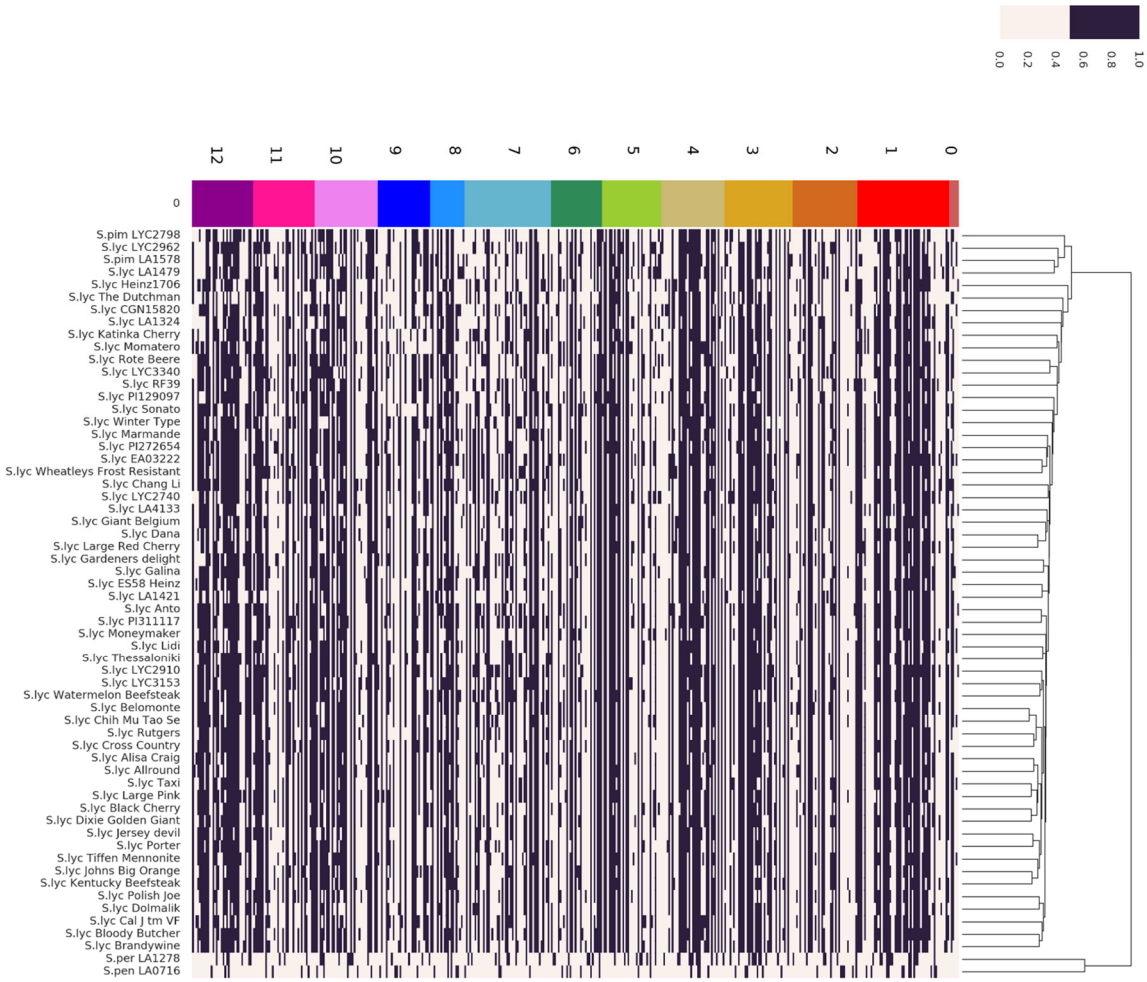

Fig. S9. Clustermap of RT50/108 insertions, with insertions ordered by chromosome position. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

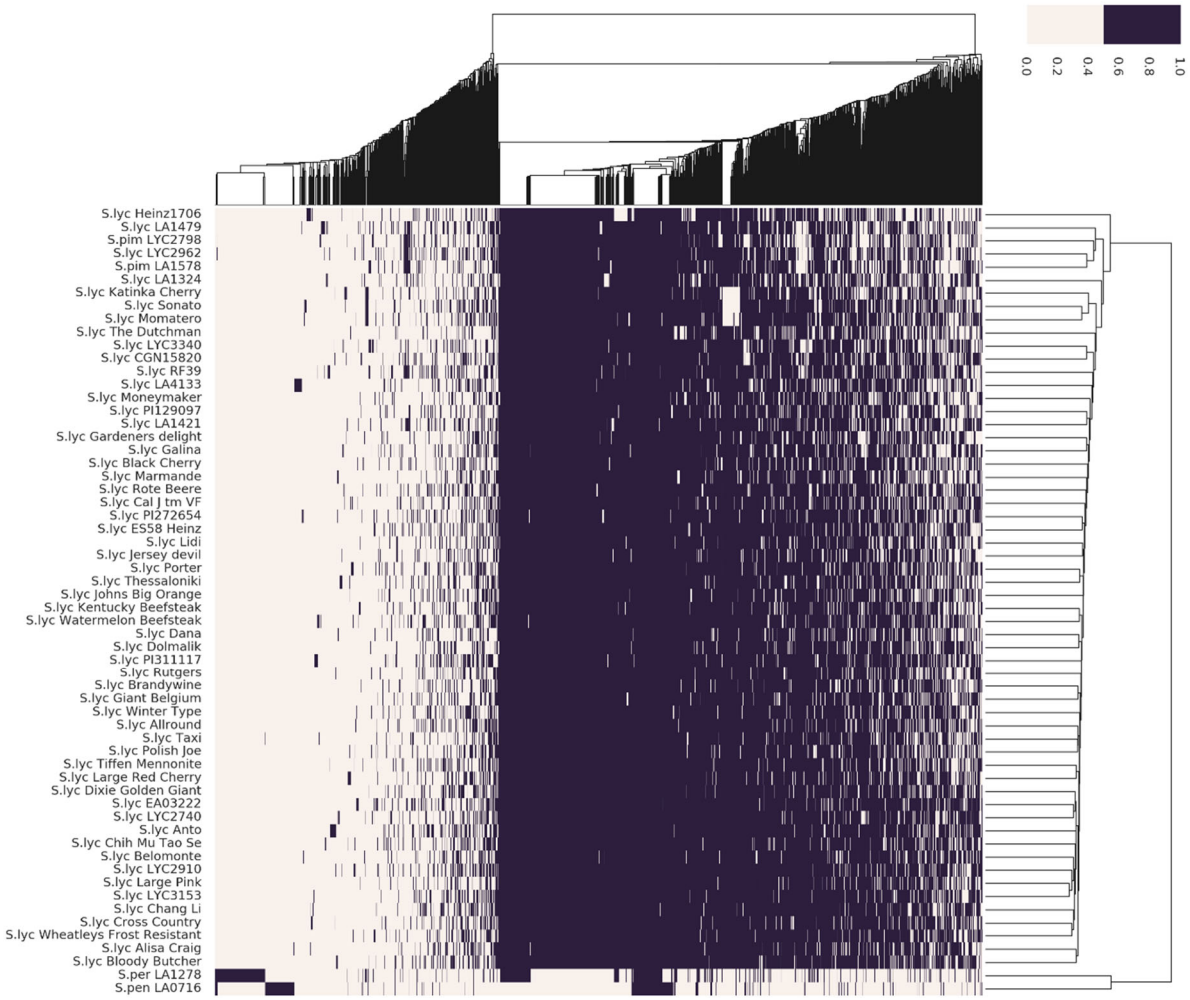

Fig. S10. Clustermap of RT_F120 insertions, with insertions clustered by Euclidian distance on the left. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

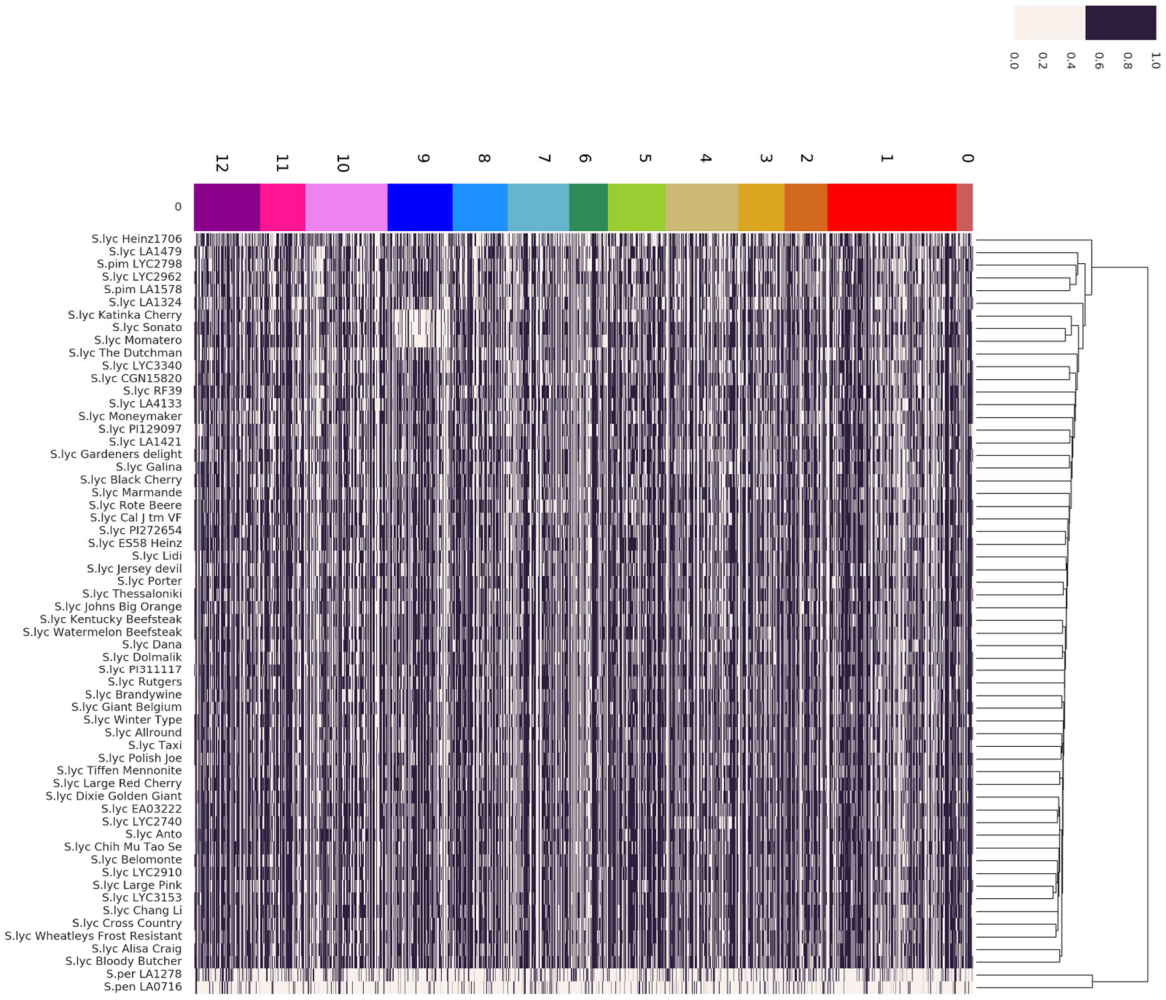

Fig. S11. Clustermap of RT_120 insertions, with insertions ordered by chromosome position. Clustering of accessions is based on Euclidian distance with regard to insertion patterns.

Table S1. Origin of the sequences of 21 RT families used for ITIS

Retrotransposon (family name)	Name	Original name	Sequence
SL_RT_F322	GypsySL_01	Jinling	Genbank:DQ445619.1
SL_RT_F160	CopiaSL_37	Rider	Genbank:EU195798.2
SL_RT_F108	CopiaSL_25		SL2.40ch01:4129840-4134803
SL_RT_F120	CopiaSL_29		SL2.40ch01:5750841-5756984
SL_RT_F132	CopiaSL_19	ToRTL1	SL2.40ch00:7052154-7061705
SL_RT_F142	CopiaSL_05		SL2.40ch01:49462910-49481696
SL_RT_F155	CopiaSL_mt		SL2.40ch03:45497629-45501747
SL_RT_F159	GypsySL_01		SL2.40ch01:56536237-56538172
SL_RT_F164	CopiaSL_33	T135	SL2.40ch01:5614665-5620194
SL_RT_F170	CopiaSL_32	Tnt1/TLC1/Retrolyc	SL2.40ch00:6887270-6892545
SL_RT_F17	GypsySL_05		SL2.40ch02:40595258-40607533
SL_RT_F204	CopiaSL_12		SL2.40ch08:43364980-43369885
SL_RT_F233	CopiaSL_14		SL2.40ch01:19673625-19679113
SL_RT_F251	CopiaSL_08		SL2.40ch01:5067307-5071046
SL_RT_F272	CopiaSL_11		SL2.40ch02:40424904-40429957
SL_RT_F274	CopiaSL_16		SL2.40ch04:30675371-30680013
SL_RT_F50	CopiaSL_38		SL2.40ch01:58925659-58930671
SL_RT_F66	CopiaSL_08		SL2.40ch01:86776883-86781925
SL_RT_F94	GypsySL_04		SL2.40ch00:4178511-4192544
	Copia_mt	TARE1	SL2.40ch01:68037445-68042819
SL_RT_F2	CopiaSL_01	TGRE1	SL2.40ch08:52147853-52152477

For the origin of retrotransposon names, refere to Table 1 in the main text

Tabel S2. Similarity matrix between RTs based on 5'and 3' sequences
percent identity matrix between LTR sequences of studied TE elements.
Comparing with reverse complement:

	Rider	SL_RT_F108	SL_RT_F120	SL_RT_F132	SL_RT_F142	SL_RT_F155	SL_RT_F159	SL_RT_F164	SL_RT_F17	SL_RT_F170	SL_RT_F204	SL_RT_F233	SL_RT_F251	SL_RT_F272	SL_RT_F274	SL_RT_F50	SL_RT_F66	SL_RT_F94	TARE1	TGRE1	
Jinling	61.8	63.8	66.6	64.4	66.8	66	63.4	66.6	66.4	63.8	65.6	65.8	64.6	65.8	64.6	64.2	64	63.8	64.4	64.6	Jinling
Rider	0	62.4	60.6	62.4	60.4	62.6	62.6	60.6	61	61.2	61.6	60.8	61.8	62	63.4	62.4	61.4	61.6	63.2	62	Rider
SL_RT_F108	0	0	65.6	65.4	65.2	65.4	65	65.6	65.4	65	66.4	66.4	66.4	65.8	67.2	98.4	67.2	65	65	64.8	SL_RT_F108
SL_RT_F120	0	0	0	65.4	65	63.8	66	65.6	65.4	64.8	66.2	65	64.4	64.8	65.4	66.6	63.8	64	63.8	65.8	SL_RT_F120
SL_RT_F132	0	0	0	0	65.2	66	65	64.8	64.8	66	66.8	65.8	65.2	66.8	66	65.2	66	65.2	64.2	65.2	SL_RT_F132
SL_RT_F142	0	0	0	0	0	65.2	64	65.4	99.4	66	66.4	65.6	65.8	65	66.4	65	65	65.6	63.2	64.2	SL_RT_F142
SL_RT_F155	0	0	0	0	0	0	65.2	64.2	65.2	64.4	65.8	65.2	65	66.6	65.8	65.2	64.8	63.4	66.4	71	SL_RT_F155
SL_RT_F159	0	0	0	0	0	0	0	66	64.2	65.2	65.6	66	65.4	66	65.8	64.4	66	63.6	64.4	63.6	SL_RT_F159
SL_RT_F164	0	0	0	0	0	0	0	0	65.2	64	64.6	65	64.2	65.8	66.6	65.4	64.6	63.8	63.6	64.2	SL_RT_F164
SL_RT_F17	0	0	0	0	0	0	0	0	0	65.2	66.4	65.8	65.2	65.2	66.2	65.2	65.2	65.6	63.4	64.2	SL_RT_F17
SL_RT_F170	0	0	0	0	0	0	0	0	0	0	65	64	65.2	65.2	65	64.8	64.8	65.2	63.4	63.8	SL_RT_F170
SL_RT_F204	0	0	0	0	0	0	0	0	0	0	0	68	68.8	71.4	70	66	69.2	66.6	66.4	65.2	SL_RT_F204
SL_RT_F233	0	0	0	0	0	0	0	0	0	0	0	0	67.6	69.4	69.6	65.8	68.2	65.4	64.6	64.8	SL_RT_F233
SL_RT_F251	0	0	0	0	0	0	0	0	0	0	0	0	0	69.4	71	66	93.6	65.6	66.8	66.4	SL_RT_F251
SL_RT_F272	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.8	66	69	65.6	65.6	64.6	SL_RT_F272
SL_RT_F274	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.8	70.6	65	68.6	67.2	SL_RT_F274
SL_RT_F50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.2	64.2	65	65.4	SL_RT_F50
SL_RT_F66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.4	67.2	66.2	SL_RT_F66
SL_RT_F94	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.4	64.4	SL_RT_F94
TARE1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.8	TARE1
TGRE1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	TGRE1

Comparing with reverse only:

	Rider	SL_RT_F108	SL_RT_F120	SL_RT_F132	SL_RT_F142	SL_RT_F155	SL_RT_F159	SL_RT_F164	SL_RT_F17	SL_RT_F170	SL_RT_F204	SL_RT_F233	SL_RT_F251	SL_RT_F272	SL_RT_F274	SL_RT_F50	SL_RT_F66	SL_RT_F94	TARE1	TGRE1	
Jinling	61.8	64	66.6	63	63.4	65.2	65.2	66.6	66.4	62.8	66.2	66.2	63	64.4	65.2	64.2	64	63.8	64.4	64.6	Jinling
Rider	0	62.6	60.6	62.6	60.2	61.4	62.6	62.2	63	61.2	61.6	61.8	61.8	60.8	63.4	62.8	61	63.4	63.4	62	Rider
SL_RT_F108	0	0	65.6	65	64.2	65	66	65.6	66.4	65.2	66.4	66.4	66	65	67.2	98.4	66.6	64.6	65	65	SL_RT_F108
SL_RT_F120	0	0	0	63.8	65	63.6	66	65.6	65.4	65	66.8	66.2	63.6	64	65.4	66.6	63.8	63.8	65.4	65.8	SL_RT_F120
SL_RT_F132	0	0	0	0	65.2	65	63.6	64.8	65.2	66	65.6	65	65.2	66.8	64.2	64.8	66	64	64.6	64.6	SL_RT_F132
SL_RT_F142	0	0	0	0	0	65.2	64	62.8	63.6	66	66.8	64.6	65.8	65	65	64	65	65.4	64.8	64.2	SL_RT_F142
SL_RT_F155	0	0	0	0	0	0	65.2	63.6	64.6	63.8	65.6	65.2	65.2	66.2	64.4	65.2	64.8	64.2	66	65.6	SL_RT_F155
SL_RT_F159	0	0	0	0	0	0	0	66	66.2	64	65.6	66	64.2	62.4	65.8	66	63.6	63.6	64.4	63.2	SL_RT_F159
SL_RT_F164	0	0	0	0	0	0	0	0	65.2	63.8	64.6	67	64	62.6	66.6	65.4	64.8	63.8	63	63.2	SL_RT_F164
SL_RT_F17	0	0	0	0	0	0	0	0	0	63.8	66.2	65.8	65	64.4	66.2	65.2	65.2	65.6	63.4	64	SL_RT_F17
SL_RT_F170	0	0	0	0	0	0	0	0	0	0	65	63.8	65.2	65.2	65	64.8	64.8	62.8	64.4	63.6	SL_RT_F170
SL_RT_F204	0	0	0	0	0	0	0	0	0	0	0	68	65.4	66	70	66	65.4	66.6	65.6	65.4	SL_RT_F204
SL_RT_F233	0	0	0	0	0	0	0	0	0	0	0	0	65.8	66.4	69.6	66	66.2	65.4	64.6	65	SL_RT_F233
SL_RT_F251	0	0	0	0	0	0	0	0	0	0	0	0	0	69.4	67.8	65.8	93.6	64	65.2	65	SL_RT_F251
SL_RT_F272	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.8	64.2	69	63.6	64.6	64.6	SL_RT_F272
SL_RT_F274	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.8	67	65	68.6	67.2	SL_RT_F274
SL_RT_F50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.2	64.8	65.2	64.4	SL_RT_F50
SL_RT_F66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.6	64.6	65.4	SL_RT_F66
SL_RT_F94	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.4	65.2	SL_RT_F94
TARE1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.8	TARE1
TGRE1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	TGRE1

Table S3. Accession numbers of tomato and wild samples.

Code	Accession name	Accession number
RF000	S.lyc Heinz1706	S.lyc LA4345
RF001	S.lyc Moneymaker	S.lyc LA2706
RF002	S.lyc Alisa Craig	S.lyc LA2838A
RF003	S.lyc Gardeners delight	S.lyc PI406760
RF004	S.lyc Rutgers	S.lyc LA1090
RF005	S.lyc Galina	S.lyc EA00325
RF006	S.lyc Taxi	S.lyc EA00488
RF007	S.lyc Katinka Cherry	S.lyc EA00375
RF008	S.lyc Johns Big Orange	S.lyc EA00371
RF011	S.lyc Allround	S.lyc LA2463
RF012	S.lyc Sonato	S.lyc LYC1969
RF013	S.lyc Cross Country	S.lyc LYC3897
RF014	S.lyc Lidi	S.lyc LYC3476
RF015	S.lyc Momatero	S.lyc TR00003
RF016	S.lyc Rote Beere	S.lyc LYC11
RF017	S.lyc RF17	S.lyc LYC3340
RF018	S.lyc Dana	S.lyc EA01155
RF019	S.lyc Large Pink	S.lyc EA01049
RF020	S.lyc RF20	S.lyc LYC3153
RF021	S.lyc RF21	S.lyc EA03222
RF022	S.lyc RF22	S.lyc PI129097
RF023	S.lyc RF24	S.lyc PI272654
RF024	S.lyc Jersey devil	S.lyc EA00990
RF026	S.lyc Polish Joe	S.lyc EA00157
RF027	S.lyc Cal J tm VF	S.lyc EA02054
RF028	S.lyc The Dutchman	S.lyc PI303721
RF029	S.lyc Black Cherry	S.lyc LA4451
RF030	S.lyc Anto	S.lyc V710029
RF031	S.lyc Winter Type	S.lyc PC11029
RF032	S.lyc Chang Li	S.lyc PI093302
RF033	S.lyc Belomonte	S.lyc EA00892
RF034	S.lyc Tiffen Mennonite	S.lyc EA01088
RF035	S.lyc Wheatleys Frost Resistant	S.lyc PI203232
RF036	S.lyc RF36	S.lyc PI311117
RF037	S.lyc RF37	S.lyc LA1324
RF038	S.lyc Chih Mu Tao Se	S.lyc PI158760
RF039	S.lyc RF39	S.lyc LA0113
RF040	S.lyc ES58 Heinz	S.lyc LYC1410
RF041	S.lyc Dolmalik	S.lyc PI169588
RF042	S.lyc RF42	S.lyc LYC2962
RF043	S.lyc RF43	S.lyc LYC2910
RF044	S.pim RF44	S.pim LYC2798
RF045	S.lyc RF45	S.lyc LYC2740
RF047	S.pim RF47	S.pim LA1578
RF049	S.per RF49	S.per LA1278
RF054	S.lyc RF54	S.lyc CGN15820
RF074	S.pen RF74	S.pen LA0716
RF077	S.lyc Large Red Cherry	S.lyc TR00018
RF078	S.lyc Porter	S.lyc EA00940
RF088	S.lyc Bloody Butcher	S.lyc TR00019
RF089	S.lyc Brandywine	S.lyc EA01019
RF090	S.lyc Dixie Golden Giant	S.lyc TR00020
RF091	S.lyc Giant Belgium	S.lyc EA01037
RF093	S.lyc Kentucky Beefsteak	S.lyc TR00021
RF094	S.lyc Marmande	S.lyc TR00022
RF096	S.lyc Thessaloniki	S.lyc TR00023
RF097	S.lyc Watermelon Beefsteak	S.lyc EA01640
RF102	S.lyc RF102	S.lyc LA4133
RF103	S.lyc RF103	S.lyc LA1421
RF105	S.lyc RF105	S.lyc LA1479
RF201	S.lyc Blondokee	EA00282
RF203	S.lyc Snowstorm	EA00470
RF206	S.lyc ABC Potato Leaf	EA00915
RF216	S.lyc Sonora	EA01985
RF226	S.lyc DL/67/248	EA05721
RF227	S.lyc Nagcarlan	EA05732
RF229	S.lyc Morne a L'Eau	EA05979
RF232	S.lyc OH88119	EA06902
RF233	S.lyc NCEBR2	EA06929
RF234	S.lyc 981136	EA06932
RF235	S.lyc Kecskemeti Koria Bibor	EA03075
RF236	S.lyc Grosse Cotelee	EA01042
RF237	S.lyc "var. cerasiforme"	EA06002
RF238	S.lyc RZ26	EA06699

Table S4. The sources of Solanaceae genomes used in this study.

Species	Common name	Source	Reference
Nicotina tabacum	tobacco	ftp://ftp.solgenomics.net/genomes/Nicotiana_tabacum/edwards_et_al_2017/assembly/Nitab-v4.5_genome_Chr_Edwards2017.fasta.gz	
Petunia axillaris	petunia	ftp://ftp.solgenomics.net/genomes/Petunia_axillaris/assembly/Petunia_axillaris_v1.6.2_genome.fasta	
Capsicum annuum cv. CM334	pepper	ftp://ftp.solgenomics.net/genomes/Capsicum_annuum/C.annuum_cvCM334/assemblies/Pepper_1.55.fasta	
Solanum tuberosum	potato	ftp://ftp.solgenomics.net/genomes/Solanum_tuberosum/assembly/PGSC_DM_v4.03/PGSC_DM_v4.03_pseudomolecules.fasta.zip	
Solanum melongena	eggplant	ftp://ftp.solgenomics.net/genomes/Solanum_melongena/SME_r2.5.1.fa.gz	
Solanum galapagense LA0436	galapagense	ftp://ftp.solgenomics.net/genomes/Solanum_galapagense/LA0436/assemblies/denovo/Sg_LA0436_denovo.fa	
Solanum arcanum LA2157	arcanum	PRJEB5226 of European Nucleotide archive (http://www.ebi.ac.uk/ena/)	Aflitos et al., 2014
Solanum habrochaites LYC4	habrochaites	PRJEB5227 of European Nucleotide archive (http://www.ebi.ac.uk/ena/)	Aflitos et al., 2014
Solanum pennellii LA0716	Pennelii (1)	PREB5228 of European Nucleotide archive (http://www.ebi.ac.uk/ena/)	Aflitos et al., 2014
Solanum pennellii LA0716	Pennelii (2)	ftp://ftp.solgenomics.net/genomes/Solanum_pennellii/Spenn.fasta	Bolger et al., 2014
Solanum pimpinellifollium LA1589	pimpinellifolium	PRJNA390234 of NCBI (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA390234/) assembly no: GCA_003660305.1	